



FIGURE 1

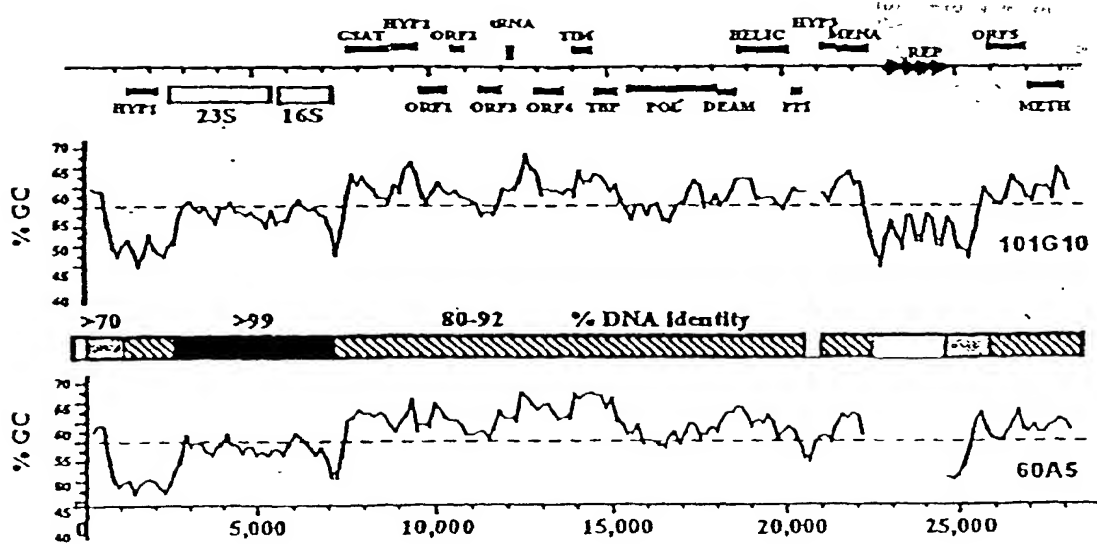


FIGURE 2

Seq Id	No	Gene	Strain	TATA Box	Coding Start	TATA to Start (bp)				
81	Hypoth 03	A	AAGCTAGACT	TTTAAT	TGGG	ATCCGGCGGG	GCGGCGCATG	-----	25	
82		B	AAGCTAAACT	TTTAAT	TGGG	ATCCGGCGAG	CCGGCGCGTG	-----		
83	Hypoth 02	A	GGAAACTTTG	ATTATA	CGGG	CGTGCTGCCC	CGGGGCCCAT	G-----	26	
84		B	GGAAACTTTG	ATTATA	CGGG	CGTACATTCC	CGGGGCCCAT	G-----		
85	ORF 02	A	AAGGCAAGGT	AATAAT	AGCC	TGCCGTCTGT	AACGGCCGTA	TG-----	27	
86		B	ACGGCAAGGT	AATAAT	AGCC	TGCCGTCCGT	ACCTGCCGTA	TG-----		
87	ORF 03	A	CATGGAACCTA	GATATT	AACC	GGTTCGCGG	ATCCCATGCA	TG-----	27	
88		B	CATGGAACCTA	GATAAT	AACC	GGTCCCGCG	GTACAATGCA	TG-----		
89	PPI	A	ATACCGAGAA	GTTATA	GCAG	GGTATGGAAT	GTGCGCGCGC	ATG-----	28	
90		B	AGCACGACAA	GTTATA	GCAG	GGTACAAAGG	AGCAGCGCAC	ATG-----		
91	GSAT	A	ATCCGCCCTG	ATTAAA	TTAT	GGGGGGAGCG	GCCTGCTGCC	GTG-----	28	
92		B	ATCCGGCCTC	ATTAAA	TTAC	GGGGGTACA	ACCTGCTGCC	GTG-----		
93	ORF 05	A	CCTTCATACA	CATAAA	TCCC	GCTTGGATGT	GCGGCTGCGC	ATG-----	28	
94		B	ACTTCATACA	CATAAA	TCCC	GCCTGAACGG	TGCTCCGCGC	ATG-----		
95	deaminase	A	GGCATATAC	CATAAT	ATGC	CGGGCGGTGG	CACCATGGCC	GTTG-----	29	
96		B	CCGCATATAC	CATAAT	ATGC	CGGGCGGGGG	CAGGCTGCCC	.GTG-----		
97	RNA helic	A	TGTACGAAAC	CATAAA	ACAA	CAGGCCGCGT	CAGGGCCGCG	CGTG-----	29	
98		B	GGGTAGAAAC	CATAAA	ACAA	CAGGCCGCGG	CAGGGCG.CG	CGTG-----		
99	ORF 06	A	ACACGCAG	TATAAA	CGGG	GGCCCGGGCG	GCGCGTATCA	CATG-----	29	
100		B	ATACACGTGG	TATAAA	CAGA	GG.CCGGACG	GCGCGGACCA	CATG-----		
101	tRNA-tyr	A	GCGATAGTTA	TTTAAA	ACTA	GGATGCCGAT	CACGGATCGT	CCCA-----	29	
102		B	GCGATAGTTA	TTTAAA	ACTA	GGATGCCGGG	CACCCGTCGT	CCCA-----		
103	TBP	A	CCGGGCCCCG	GTAAAA	ATAG	CG.CACGGGC	GGATCCTGAC	CAATG-----	30	
104		B	CCGGGCCCCG	GTAAAA	ATAG	AGTGCGGCCG	GGCACCGGAT	CAATG-----		
105	TIH	A	GCGTCGATAG	AATAAA	TACG	CGCAGGGGGC	CCCCTGGCGC	GATCGCCCGT	G-----	36
106		B	GCGTCGATAG	AATAAA	TACG	CGC.GGGGCC	GCGGTGC...	GATCGCCCGT	G-----	
107	Hypoth 01	A	ATTTCAACTA	CATAAA	TGCC	TAGTTACGCA	GAAATAGCAA	ACGACGTACT	TCGACTAATG	45
108		B	ACTTCAACTA	CATAAA	TGCC	TAGCTACGCA	GAAATATCAA	ACAAAGTACT	TCGACTAATG	
109	ORF 01	A	ACGGCAGGCT	ATTATT	ACCT	TGCCCTGCGT	TGTA //..G	CGGGGTGCGG	CAGGGGATG	52
110		B	ACGGCAGGCT	ATTATT	ACCT	TGCCGTGTG.	TACA //..G	AGGGGGCCTG	CCGGGAGTG	
111	Methylase	A	CTACAACGAT	TTTAAG	TCCG	CGCCGGGGCA	GCCG.//..G	ATGTGGGGCA	GGCAACATG	104
112		B	CTACAAAGAT	TTTAAG	ACGG	CGCGGGTGCC	GCCG.//..T	GGCACGGGGG	CCTATCTTG	
113	16S RNA	A	TCCGCGATGG	TTTATA	TGCC	CATGGACGGG	CCGATCCGAT	CGTACGTGAC	GC.//..AAT	220
114		B	CCGGCGATGG	TTTATA	TGCC	CATGGACAAG	GCGATCCGAT	CGTACGTGAC	GC.//..AAT	
	Archaeal promoter consensus			YTTAAWA						

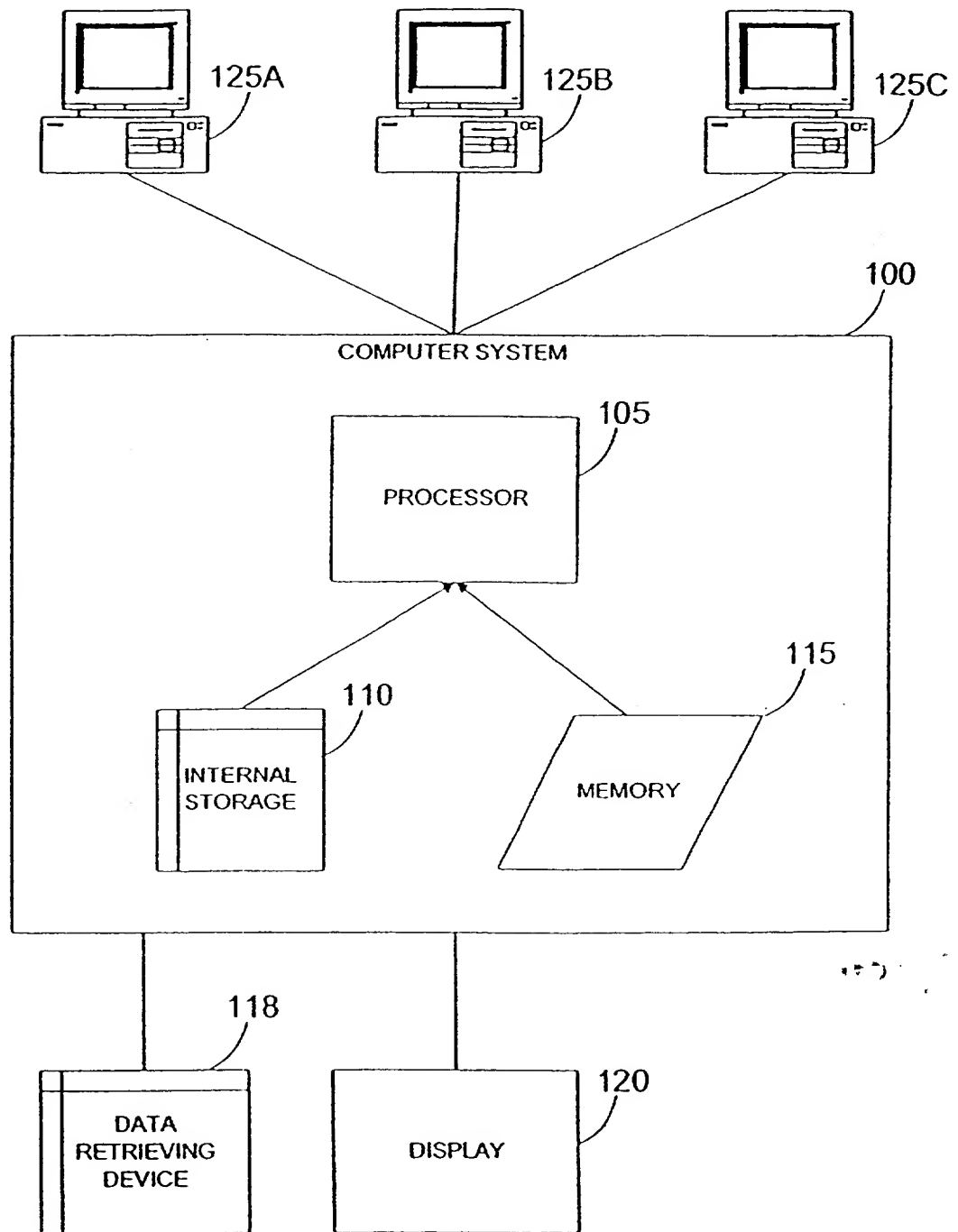


FIGURE 3

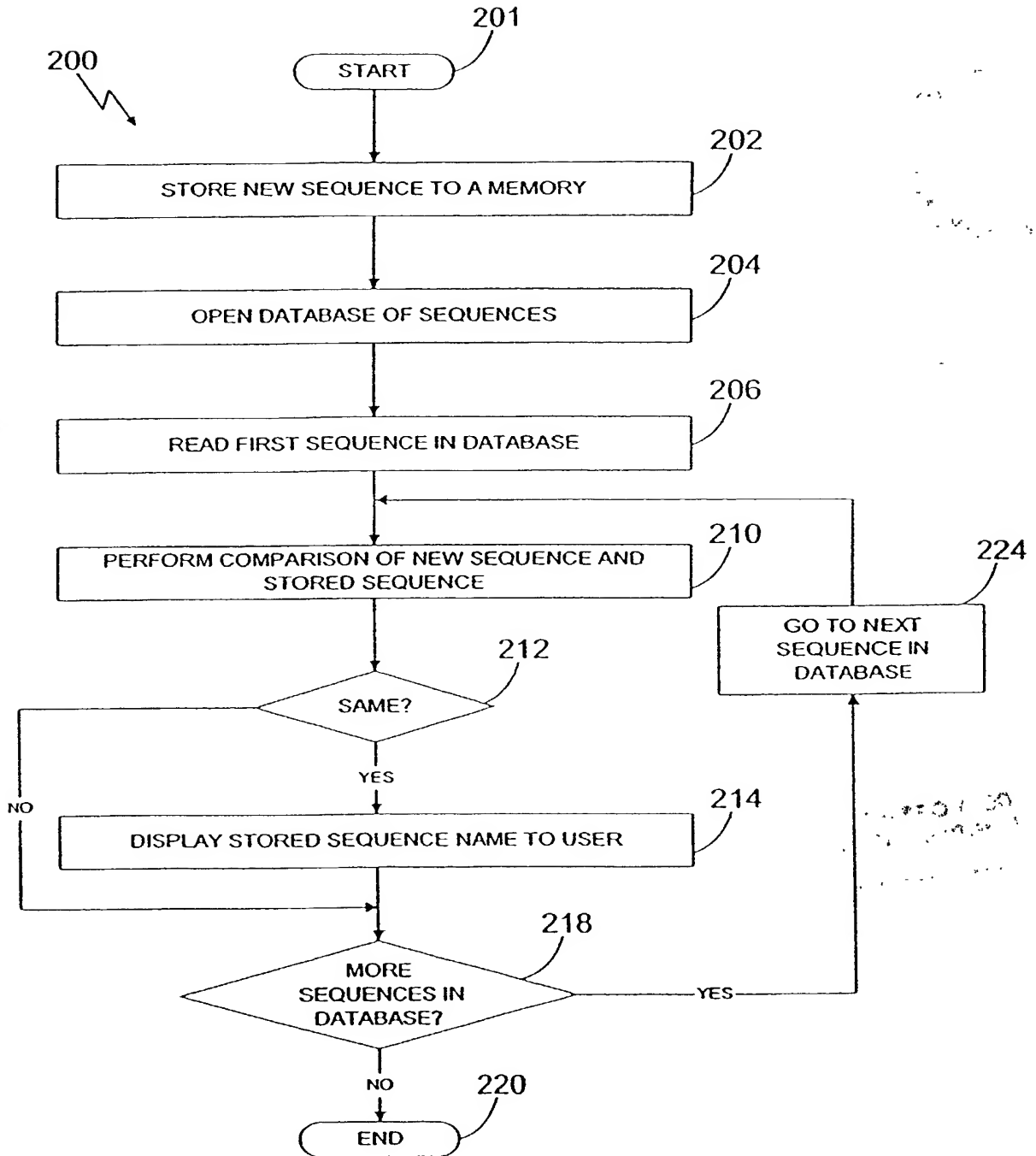
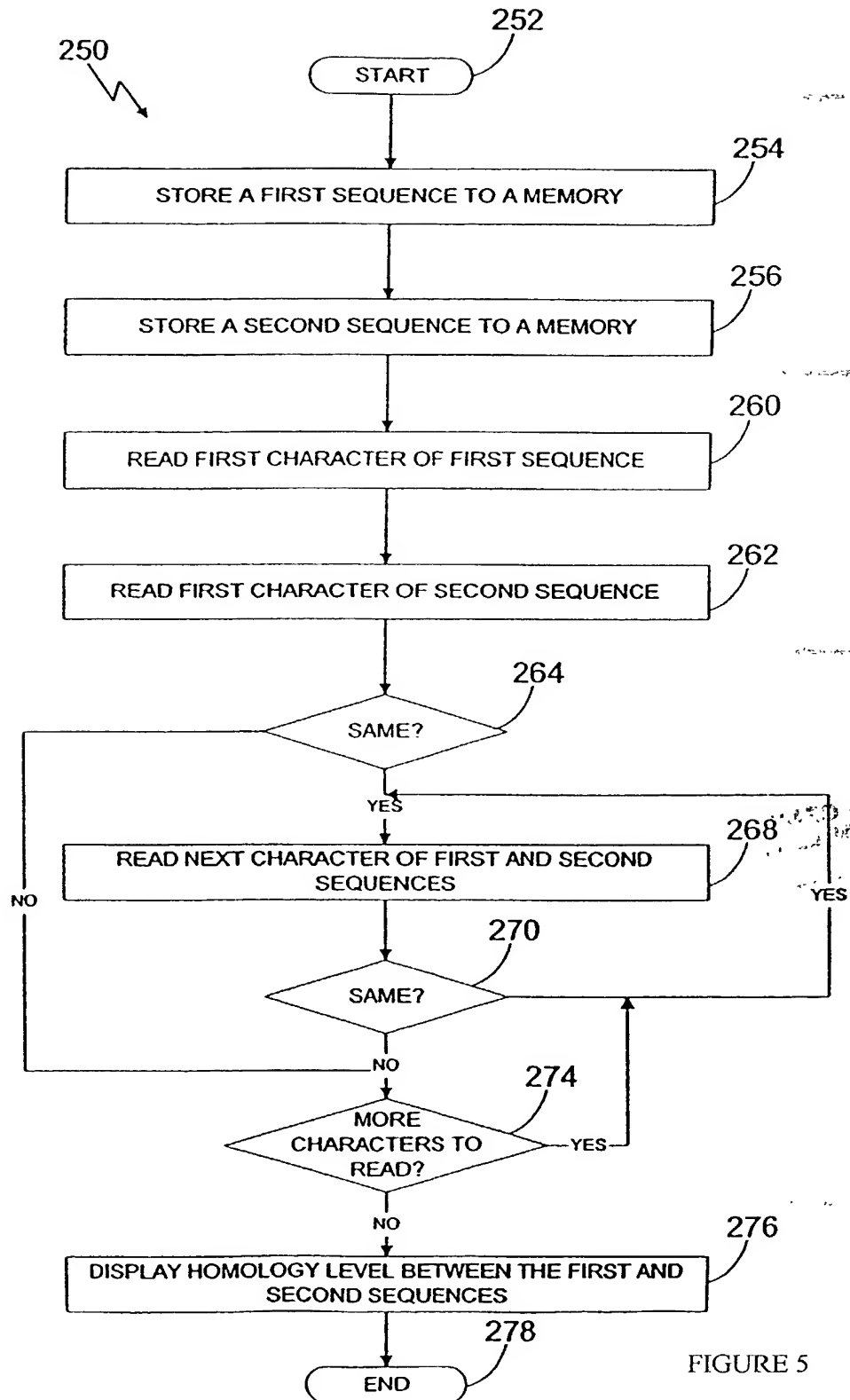


FIGURE 4



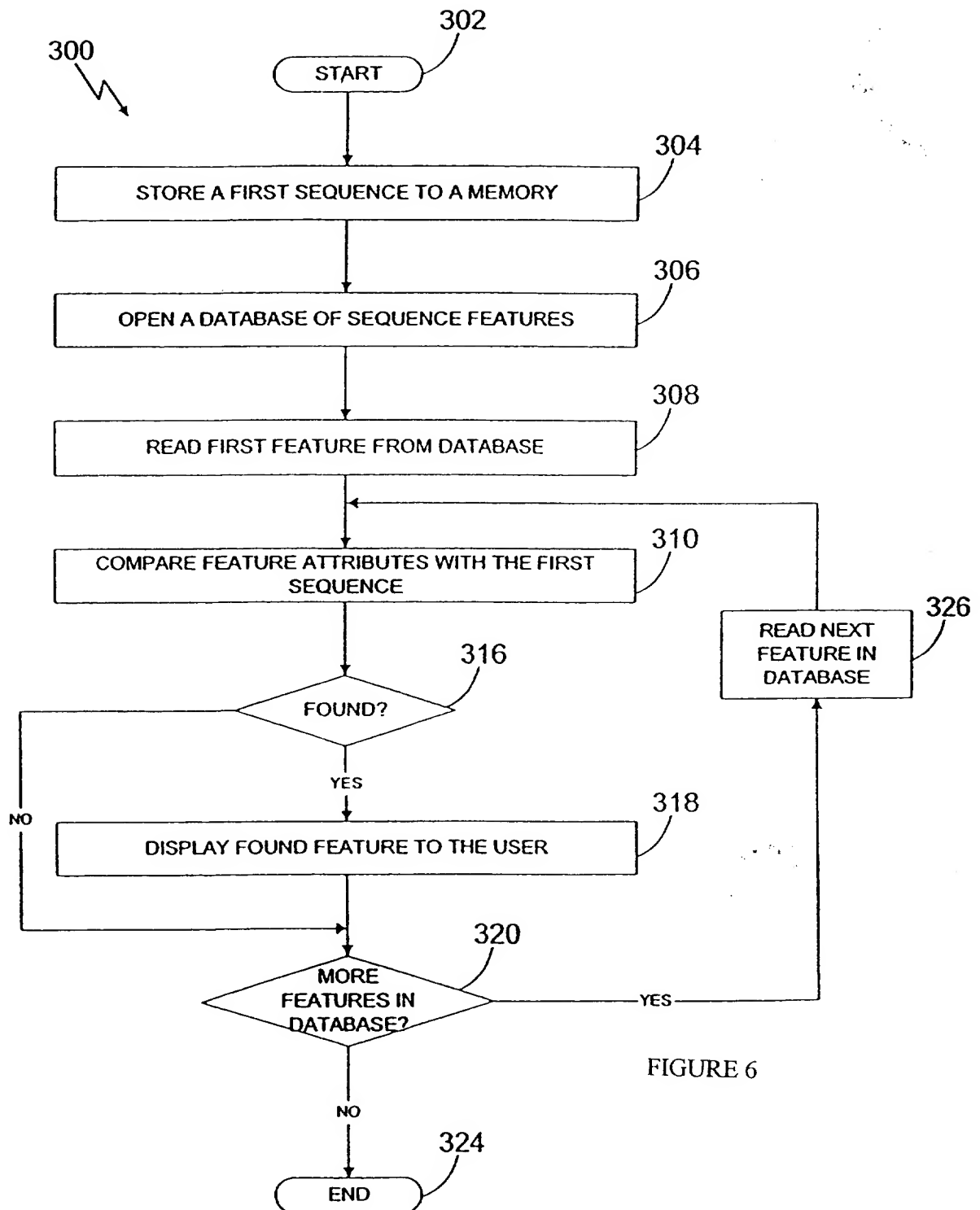


FIGURE 6